

#9

1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,458

DATE: 12/28/2001

TIME: 16:10:51

Input Set : A:\13198.asc

Output Set: N:\CRF3\12282001\I424458.raw

TECH CENTER 1600/2900

JAN 10 2002

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ENTERED

Need to logout.
01/09/02

4 <110> APPLICANT: Hayward, Nicholas
 5 Silins, Ginters
 6 Grimmond, Sean
 7 Gartside, Michael
 8 Hancock, John
 10 <120> TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
 12 <130> FILE REFERENCE: 13198
 14 <140> CURRENT APPLICATION NUMBER: 09/424,458
 15 <141> CURRENT FILING DATE: 2000-03-16
 17 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00380
 18 <151> PRIOR FILING DATE: 1998-05-22
 20 <160> NUMBER OF SEQ ID NOS: 111
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 8
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide repeat
 31 motif in DnaJ homologues.
 33 <220> FEATURE:
 34 <221> NAME/KEY: UNSURE
 35 <222> LOCATION: (2)..(3)
 36 <223> OTHER INFORMATION: Xaa at position 2,3 can be any amino acid.
 38 <220> FEATURE:
 39 <221> NAME/KEY: UNSURE
 40 <222> LOCATION: (5)
 41 <223> OTHER INFORMATION: Xaa at position 5 can be any amino acid.
 43 <220> FEATURE:
 44 <221> NAME/KEY: UNSURE
 45 <222> LOCATION: (7)
 46 <223> OTHER INFORMATION: Xaa at position 7 can be any amino acid.
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 49 Cys Xaa Xaa Cys Xaa Gly Xaa Gly
 50 1 5
 53 <210> SEQ ID NO: 2
 54 <211> LENGTH: 1242
 55 <212> TYPE: DNA
 56 <213> ORGANISM: Homo sapiens
 58 <220> FEATURE:
 59 <221> NAME/KEY: CDS
 60 <222> LOCATION: (30)..(959)
 62 <400> SEQUENCE: 2
 63 tcagtaaaca cagagactgg ggatcgatc atg ggg ctt tgt aag tgc ccc aag 53
 65 Met Gly Leu Cys Lys Cys Pro Lys
 66 1 5
 68 aga aag gtg acc aac ctg ttc tgc ttc gaa cat cgg gtc aac gtc tgc 101

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70 Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn Val Cys
71      10                      15                      20
73 gag cac tgc ctg gta gcc aat cac gcc aag tgc atc gtc cag tcc tac   149
75 Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln Ser Tyr
76  25                      30                      35                      40
78 ctg caa tgg ctc caa gat agc gac tac aac ccc aat tgc cgc ctg tgc   197
80 Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg Leu Cys
81                      45                      50                      55
83 aac ata ccc ctg gcc agc cga gag acg acc cgc ctt gtc tgc tat gat   245
85 Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys Tyr Asp
86                      60                      65                      70
88 ctc ttt cac tgg gcc tgc ctc aat gaa cgt gct gcc cag cta ccc cga   293
90 Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg
91                      75                      80                      85
93 aac acg gca cct gcc ggc tat cag tgc ccc agc tgc aat ggc ccc atc   341
95 Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ile
96  90                      95                      100
98 ttc ccc cca acc aac ctg gct ggc ccc gtg gcc tcc gca ctg aga gag   389
100 Phe Pro Pro Thr Asn Leu Ala Gly Pro Val Ala Ser Ala Leu Arg Glu
101 105                      110                      115                      120
103 aag ctg gcc aca gtc aac tgg gcc cgg gca gga ctg ggc ctc cct ctg   437
105 Lys Leu Ala Thr Val Asn Trp Ala Arg Ala Gly Leu Gly Leu Pro Leu
106                      125                      130                      135
108 atc gat gag gtg gtg agc cca gag ccc gag ccc ctc aac acg tct gac   485
110 Ile Asp Glu Val Val Ser Pro Glu Pro Glu Pro Leu Asn Thr Ser Asp
111                      140                      145                      150
113 ttc tct gac tgg tct agt ttt aat gcc agc agt acc cct gga cca gag   533
116 Phe Ser Asp Trp Ser Ser Phe Asn Ala Ser Ser Thr Pro Gly Pro Glu
117                      155                      160                      165
119 gag gta gac agc gcc tct gct gcc cca gcc ttc tac agc cga gcc ccc   581
121 Glu Val Asp Ser Ala Ser Ala Ala Pro Ala Phe Tyr Ser Arg Ala Pro
122                      170                      175                      180
124 cgg ccc cca gct tcc cca ggc cgg ccc gag cag cac aca gtg atc cac   629
126 Arg Pro Pro Ala Ser Pro Gly Arg Pro Glu Gln His Thr Val Ile His
127 185                      190                      195                      200
129 atg ggc aat cct gag ccc ttg act cac gcc cct agg aag gtg tat gat   677
131 Met Gly Asn Pro Glu Pro Leu Thr His Ala Pro Arg Lys Val Tyr Asp
132                      205                      210                      215
134 acg cgg gat gat gac cgg aca cca ggc ctc cat gga gac tgt gac gat   725
136 Thr Arg Asp Asp Asp Arg Thr Pro Gly Leu His Gly Asp Cys Asp Asp
137                      220                      225                      230
139 gac aag tac cga cgt cgg ccg gcc ttg ggt tgg ctg gcc cgg ctg cta   773
141 Asp Lys Tyr Arg Arg Arg Pro Ala Leu Gly Trp Leu Ala Arg Leu Leu
142                      235                      240                      245
144 agg agc cgg gct ggg tct cgg aag cgg ccg ctg acc ctg ctc cag cgg   821
146 Arg Ser Arg Ala Gly Ser Arg Lys Arg Pro Leu Thr Leu Leu Gln Arg
147                      250                      255                      260
149 gcg ggg ctg ctg cta ctc ttg gga ctg ctg ggc ttc ctg gcc ctc ctt   869
151 Ala Gly Leu Leu Leu Leu Leu Gly Leu Leu Gly Phe Leu Ala Leu Leu

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152 265          270          275          280
154 gcc ctc atg tct cgc cta ggc cgg gcc gca gct gac agc gat ccc aac 917
156 Ala Leu Met Ser Arg Leu Gly Arg Ala Ala Ala Asp Ser Asp Pro Asn
157          285          290          295
159 ctg gac cca ctc atg aac cct cac atc cgc gtg ggc ccc tcc 959
161 Leu Asp Pro Leu Met Asn Pro His Ile Arg Val Gly Pro Ser
162          300          305          310
164 tgagccccct tgcttgtggc taggccagcc taggatgtgg gttctgtgga ggagaggcgg 1019
167 ggtaatgggg aggctgaggg cacctcttca ctgcccctct ccctcaagcc taagacacta 1079
170 agaccccaga cccaaagcca agtccaccag agtggctcgc aggccaggcc tggagtcccc 1139
173 gtgggtcaag catttgtctt gacttgcttt ctcccgggtc tccagcctcc gacccctcgc 1199
176 cccatgaagg agctggcagg tggaaataaa caacaacttt att 1242
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 310
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 3
186 Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys
187 1 5 10 15
189 Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His
190 20 25 30
192 Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp
193 35 40 45
195 Tyr Asn Pro Asn Cys Arg Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu
196 50 55 60
198 Thr Thr Arg Leu Val Cys Tyr Asp Leu Phe His Trp Ala Cys Leu Asn
199 65 70 75 80
201 Glu Arg Ala Ala Gln Leu Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln
202 85 90 95
204 Cys Pro Ser Cys Asn Gly Pro Ile Phe Pro Pro Thr Asn Leu Ala Gly
205 100 105 110
207 Pro Val Ala Ser Ala Leu Arg Glu Lys Leu Ala Thr Val Asn Trp Ala
208 115 120 125
210 Arg Ala Gly Leu Gly Leu Pro Leu Ile Asp Glu Val Val Ser Pro Glu
211 130 135 140
213 Pro Glu Pro Leu Asn Thr Ser Asp Phe Ser Asp Trp Ser Ser Phe Asn
214 145 150 155 160
216 Ala Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser Ala Ser Ala Ala
217 165 170 175
219 Pro Ala Phe Tyr Ser Arg Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg
220 180 185 190
222 Pro Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr
223 195 200 205
226 His Ala Pro Arg Lys Val Tyr Asp Thr Arg Asp Asp Asp Arg Thr Pro
227 210 215 220
230 Gly Leu His Gly Asp Cys Asp Asp Asp Lys Tyr Arg Arg Arg Pro Ala
231 225 230 235 240
233 Leu Gly Trp Leu Ala Arg Leu Leu Arg Ser Arg Ala Gly Ser Arg Lys
234 245 250 255

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```

236 Arg Pro Leu Thr Leu Leu Gln Arg Ala Gly Leu Leu Leu Leu Leu Gly
237          260          265          270
239 Leu Leu Gly Phe Leu Ala Leu Leu Ala Leu Met Ser Arg Leu Gly Arg
240          275          280          285
242 Ala Ala Ala Asp Ser Asp Pro Asn Leu Asp Pro Leu Met Asn Pro His
243          290          295          300
245 Ile Arg Val Gly Pro Ser
246 305          310
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 2415
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (3)..(2186)
260 <400> SEQUENCE: 4
261 cg att tca ttc ctc gct ccc cac agg tcc ctc tcc cca aaa tat tcc 47
263   Ile Ser Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser
264     1          5          10          15
266 cat ctt gtc cta gcc cat ccc cca gac tat ctc aag gac cag ctg tcc 95
268 His Leu Val Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser
269          20          25          30
271 cca cgc ccc cga cct cca cta ggc ctg tgc cac ccg ctg cct gca gga 143
273 Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly
274          35          40          45
276 aga cgc ccg gtc ccg ggc cgg gtt agc ccc atg gga acg cag cgc ctg 191
278 Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu
279          50          55          60
281 tgt ggc cgc ggg act caa ggc tgg cct ggc tca agt gaa cag cac gtc 239
283 Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val
284          65          70          75
286 cag gag gcg acc tcg tcc gcg ggt ttg cat tct ggg gtg gac gag ctg 287
288 Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu
289 80          85          90          95
291 ggg gtt cgg tcc gag ccc ggt ggg agg ctc ccg gag cgc agc ctg ggc 335
293 Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly
294          100          105          110
296 cca gcc cac ccc gcg ccg gcg gcc atg gca ggc acc ctg gac ctg gac 383
298 Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp
299          115          120          125
301 aag ggc tgc acg gtg gag gag ctg ctc cgc ggg tgc atc gaa gcc ttc 431
303 Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys Ile Glu Ala Phe
304          130          135          140
306 gat gac tcc ggg aag gtg cgg gac ccg cag ctg gtg cgc atg ttc ctc 479
308 Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu
309          145          150          155
311 atg atg cac ccc tgg tac atc ccc tcc tct cag ctg gcg gcc aag ctg 527
313 Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu
314 160          165          170          175

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```

316 ctc cac atc tac caa caa tcc cgg aag gac aac tcc aat tcc ctg cag 575
318 Leu His Ile Tyr Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln
319      180      185      190
321 gtg aaa acg tgc cac ctg gtc agg tac tgg atc tcc gcc ttc cca gcg 623
323 Val Lys Thr Cys His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala
324      195      200      205
326 gag ttt gac ttg aac ccg gag ttg gct gag cag atc aag gag ctg aag 671
328 Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys
329      210      215      220
331 gct ctg cta gac caa gaa ggg aac cga cgg cac agc agc cta atc gac 719
333 Ala Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp
334      225      230      235
336 ata gac agc gtc cct acc tac aag tgg aag cgg cag gtg act cag cgg 767
338 Ile Asp Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg
339 240      245      250      255
341 aac cct gtg gga cag aaa aag cgc aag atg tcc ctg ttg ttt gac cac 815
343 Asn Pro Val Gly Gln Lys Lys Arg Lys Met Ser Leu Leu Phe Asp His
344      260      265      270
346 ctg gag ccc atg gag ctg gcg gag cat ctc acc tac ttg gag tat cgc 863
348 Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr Leu Glu Tyr Arg
349      275      280      285
351 tcc ttc tgc aag atc ctg ttt cag gac tat cac agt ttc gtg act cat 911
353 Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser Phe Val Thr His
354      290      295      300
356 ggc tgc act gtg gac aac ccc gtc ctg gag cgg ttc atc tcc ctc ttc 959
358 Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe
359      305      310      315
361 aac agc gtc tca cag tgg gtg cag ctc atg atc ctc agc aaa ccc aca 1007
363 Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr
364 320      325      330      335
366 gcc ccg cag cgg gcc ctg gtc atc aca cac ttt gtc cac gtg gcg gag 1055
368 Ala Pro Gln Arg Ala Leu Val Ile Thr His Phe Val His Val Ala Glu
369      340      345      350
371 aag ctg cta cag ctg cag aac ttc aac acg ctg atg gca gtg gtc ggg 1103
373 Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met Ala Val Val Gly
374      355      360      365
376 ggc ctg agc cac agc tcc atc tcc cgc ctc aag gag acc cac agc cac 1151
378 Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu Thr His Ser His
379      370      375      380
381 gtt agc cct gag acc atc aag ctc tgg gag ggt ctc acg gaa cta gtg 1199
383 Val Ser Pro Glu Thr Ile Lys Leu Trp Glu Gly Leu Thr Glu Leu Val
384      385      390      395
386 acg gcg aca ggc aac tat ggc aac tac cgg cgt cgg ctg gca gcc tgt 1247
388 Thr Ala Thr Gly Asn Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys
389 400      405      410      415
391 gtg ggc ttc cgc ttc ccg atc ctg ggt gtg cac ctc aag gac ctg gtg 1295
393 Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val
394      420      425      430
396 gcc ctg cag ctg gca ctg cct gac tgg ctg gac cca gcc cgg acc cgg 1343

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

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L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:2257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76